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**ELSEVIER SCIENCE
FULL-TEXT ARTICLE**

The tax gene sequences form two divergent monophyletic lineages corresponding to types I and II of simian and human T-cell leukemia/lymphotropic viruses.

Giri A, Slattery JP, Heneine W, Gessain A, Rivadeneira E, Desrosiers RC, Rosen L, Anthony R, Pamungkas J, Iskandriati D, Richards AL, Herve V, McClure H, O'Brien SJ, Franchini G.

Basic Research Laboratory, National Cancer Institute, Bethesda, Maryland 20892, USA.

Evolutionary associations of human and simian T-cell leukemia/lymphotropic viruses I and II (HTLV-I/II and STLV-I/II) are inferred from phylogenetic analysis of tax gene sequences. Samples studied consisted of a geographically diverse assemblage of viral strains obtained from 10 human subjects and 20 individuals representing 12 species of nonhuman primates. Sequence analyses identified distinct substitutions, which distinguished between viral types I and II, irrespective of host species. Phylogenetic reconstruction of nucleotide sequences strongly supported two major evolutionary groups corresponding to viral types I and II. With the type I lineage, clusters were composed of strains from multiple host species. A genetically diverse, monophyletic lineage consisting of eight new viral strains from several species of Asian macaques was identified. The second lineage consisted of a monophyletic assemblage of HTLV-II/STLV-II strains from Africa and the New World, including an isolate from a pygmy chimp (*Pan paniscus*) as an early divergence within the lineage. High levels of genetic variation among strains from Asian STLV-I macaque suggest the virus arose in Asia. Evidence of the origin of the type II virus is less clear,

but diversity among HTLV-II variants from a single isolated population of Mbati villagers is suggestive but not proof of an African origin.

PMID: 9143307 [PubMed - indexed for MEDLINE]

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